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13. ABSTRACT (Maximum 200 Words) <p>Identification of proteins involved in the initiation of disease and the identification of small molecules that can modulate these proteins are of great importance towards the discovery of treatments for human chemotherapy. For example, compounds that potentiate estrogen receptor-mediated gene expression comprise a large class of currently employed chemotherapeutics. These compounds are employed to both treat breast cancer and provide hormone replacement therapy. Although initially beneficial, over time current clinically prescribed compounds can exhibit deleterious side-effects that include the development of drug resistance and an increased risk of breast cancer.</p> <p>We initially hypothesized that a recently described genetic system termed split-intein mediated circular ligation of peptides and proteins (SICLOPPS) (PNAS, 1999, 96, 13638-13643) could enable the identification of small cyclic peptides that exhibit estrogenic and antiestrogenic activity in recombinant yeast systems. However, preliminary data suggests that SICLOPPS does not function or express well in yeast. Current efforts are directed at using related systems to investigate oncogenic protein tyrosine kinases and to identify estrogenic proteins. These investigations may identify and potentiate critical protein interactions involved in the proliferation of breast cancer.</p>				
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(Reprint of D. D. Clark, B. R. Peterson, <i>ChemBioChem</i> 2003 , 4, 101-107)	

Research Summary:

Protein-protein interactions are critical elements of cellular mechanisms for survival. Permutations in these otherwise highly controlled interactions can promote or prevent human disease state(s). Identification of proteins involved in the initiation of disease and the identification of small molecules that can potentiate these proteins are of great importance towards the discovery of treatments for human chemotherapy. This proposal is directed at identifying methods to identify and to potentiate critical protein interactions involved in the proliferation of breast cancer.

The human estrogen receptor (ER) has been identified as a key protein involved in the proliferation of breast cancer and is a target of breast cancer chemotherapies. The estrogen receptor (ER) α and β subtypes are hormone-inducible nuclear receptors that regulate gene expression upon binding estrogens such as the steroid hormone β -estradiol (E_2). These binding events control consequent protein-protein interaction pathways vital for development and cellular proliferation.

ER-positive breast cancers are vulnerable to estrogen receptor antagonists termed antiestrogens, which block breast cancer cell proliferation by competitively inhibiting E_2 binding to ERs.^[1, 2] First line therapy with antiestrogens such as tamoxifen effectively stops cancer cell growth in the majority of ER-positive breast cancers.^[3] ⁴⁾ Unfortunately, breast cancers inevitably become resistant to antiestrogen chemotherapy^[4, 5] and considerable evidence exists that the antiestrogen tamoxifen can eventually cause endometrial cancer in premenopausal women.^[6]

Conversely, it has been recognized that postmenopausal women, who no longer produce estrogenic hormones due to decreased ovarian function, can benefit from hormone replacement therapy (HRT), which primarily consists of a regime of estrogens. HRT has been shown to reduce mortality in postmenopausal women as a consequence of coronary heart disease and osteoporosis.^[3] However, emerging evidence suggests that HRT confers an increased risk of breast cancer in these patients.^[7]

We proposed to test the hypothesis that combinatorial chemical libraries of cyclic peptides expressed in yeast using the recently described split-intein mediated circular ligation of peptides and proteins (SICLOPPS) genetic system^[8] will yield potent, stable, and cell-permeable modulators of ER-mediated gene expression. These compounds were designed based on Segetalin natural products, which are cyclic peptides that exhibit estrogenic activity in animals.^[9-11] Promising compounds could be evaluated in whole-cell assays in an attempt to identify novel compounds with potential activity as chemotherapies for breast cancer or for hormone replacement.

As described in the statement of work, Task 1 involved the construction, expression and screening of the SICLOPPS combinatorial library of Segetalin H-mimetic cyclic peptides in yeast to identify potential estrogens and antiestrogens for the duration of the first year of this funding. Unfortunately, the construction of a functional SICLOPPS system in yeast proved more difficult than initially hypothesized. Preliminary experiments employed green fluorescent protein (GFP) and were directed at the validation of SICLOPPS expression and function in yeast. In these experiments the synthesis of excised, cyclic GFP from the SICLOPPS system in yeast could be evaluated by immunoblotting and fluorescence microscopy techniques. However, the SICLOPPS system employed for this work demonstrated low expression and no detectable function in yeast. It was hypothesized that since the SICLOPPS system was isolated from a bacterial strain it may not express well in yeast. To evaluate

the integrity of the SICLOPPS constructs, analogous SICLOPPS constructs were prepared for examination in bacteria. In bacteria these SICLOPPS constructs expressed and functioned properly, providing evidence that the SICLOPPS constructs were assembled correctly, but would not function adequately in yeast to continue with this proposed work.

Although the SICLOPPS system failed in the preliminary stages, my graduate work has focused on investigating protein-protein interactions, in yeast genetic systems, towards increased understanding of these molecular bases of disease. One successful project that has been under investigation involves the reconstitution of protein tyrosine kinase (PTK) initiated protein-protein interactions in a recombinant yeast system. PTKs catalyze the transfer of the gamma phosphate of ATP to specific tyrosine residues of target proteins to initiate protein-protein interactions that transmit signals to the cell nucleus for vast cellular functions. More importantly aberrant PTK activity has been implicated in numerous human disease states, including breast cancer. Through investigation of Abl and Src as model PTKs, I developed a yeast tribrid system employing a potentially universal PTK substrate that could be employed as a high-throughput screening method to identify compounds that inhibit PTK activity or as a proteomic tool to identify novel PTKs that could be involved in disease.^[12] Furthermore, I modified this system to identify chemotherapeutically relevant compounds that inhibit PTK activity (Appendix).^[13] Modifications in this system could be useful to investigate compounds with ability to inhibit PTKs specific to breast cancer proliferation. Currently, I am investigating this yeast tribrid assay coupled with a recently designed fluorescence-based reporter gene assay towards screening of a human cDNA library to discover proteins with PTK activity. This type of screen could lead to the discovery of previously uncharacterized proteins that have roles in the progression of breast cancer.

Another ongoing project involves adapting a recently reported yeast three-hybrid system, developed in our laboratory,^[14] to screen a human cDNA library for proteins that bind to E_2 . This system involves the use of a chemical inducer of dimerization (CID) that serves to dimerize the engineered biotin-binding protein streptavidin with the engineered E_2 -binding protein hER to activate reporter gene expression. We hypothesize that this system could be employed in conjunction with a recently designed fluorescence-based reporter gene as a facile means to determine a variety of ligand-protein interactions. For example, this system could be utilized to identify isoforms of hER or other proteins involved in breast cancer proliferation from a cDNA library with the previously synthesized E_2 -Biotin compound.^[14] Furthermore, we hypothesize that biotinylation of a wide range of natural product small-molecules could serve to identify cognate proteins that could be pharmacologically relevant.

In conclusion, the research during this first year of funding has revealed that the SICLOPPS system does not express or function well in yeast. However, we are using related genetic systems to investigate proteins involved in breast cancer proliferation.

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Key Research Accomplishments:

Evaluation of SICLOPPS:

- Examined the utility of SICLOPPS system in yeast genetic systems.
- Modified and utilized a number of hER-based yeast hybrid systems towards detection of estrogenic compounds.

Investigations of oncogenic PTKs:

- Adapted a previously reported yeast tribrid system employing a universal PTK substrate for high-throughput screening for known PTK inhibitors.
- Developed a new yeast strain (DCY250) that is permeable to a wide range of compounds.
- Identified PTK inhibitors with the yeast tribrid technology.

Development of a yeast fluorescent reporter gene:

- Designed and evaluated a yeast fluorescent reporter gene that could be combined with flow cytometry to evaluate reporter gene expression.
- Implemented the reporter for use in various breast cancer relevant systems.

Reportable Outcomes:

Manuscripts:

Clark, D. D. and Peterson, B. R. "Analysis of Protein Tyrosine Kinase Inhibitors in Recombinant Yeast Lacking the *ERG6* Gene" *ChemBioChem* **2003**, *4*, 101-107.

Abstract: Studies of small molecule-protein interactions in yeast can be hindered by the limited permeability of yeast to small molecules. This diminished permeability is thought to be related to the unique sterol composition of fungal membranes, which are enriched in the steroid ergosterol. We report the construction of the novel yeast strain DCY250 that is compatible with yeast two hybrid-based systems and bears a targeted disruption of the *ERG6* gene to ablate ergosterol biosynthesis and enhance permeability to small molecules. The small molecule inhibitors of protein tyrosine kinases (PTKs) PP1, PP2, herbimycin A, and staurosporine were investigated with yeast tribrid systems that detect the activity of the PTKs v-Abl and v-Src. These tribrid systems function by expressing the PTK, a B42 activation domain fused to the phosphotyrosine-binding Grb2 SH2 domain, a DNA-bound LexA-GFP-(AAYANAA)₄ universal PTK substrate, and a *lacZ* reporter gene. Yeast genetic systems lacking functional *ERG6* were found to be as much as 20-fold more sensitive to small molecule inhibitors of PTKs, and these systems may provide a useful platform for the discovery and analysis of small molecule-protein interactions.

Presentations:

Clark, D. D. and Peterson B. R. "Analysis of Oncogenic Protein Tyrosine Kinases Expressed in Recombinant Yeast" *Biochemistry*. **2002**, *41*(28), 29. (Poster presented at the 224th American Chemical Society National Meeting; Boston, Massachusetts; August 18-22, 2002.)

Abstract: Yeast two-hybrid systems are powerful proteomics tools for the discovery and characterization of protein-protein interactions. However, these systems are typically unable to detect interactions dependent on post-translational modifications such as tyrosine phosphorylation. We report a novel yeast tribrid system that expresses a potentially universal protein tyrosine kinase (PTK) substrate to detect diverse PTKs. Validation with the oncogenic kinases v-Abl and v-Src, which exhibit divergent substrate specificities, demonstrated significant potential for cloning PTKs en masse from cDNA libraries. This approach also has potential for the discovery of small molecules that modulate PTK activity. Recent efforts to analyze synthetic and natural inhibitors of PTKs with recombinant yeast-based assays will be described.

Travel Award:

Clark, D. D. American Chemical Society Division of Biological Chemistry Travel Award (2002) (Provided funding to travel to the 224th American Chemical Society National Meeting; Boston MA; August 18-22, 2002)

Revised Statement of Work:

Task 1: Design and evaluate a yeast fluorescent reporter gene. (Months 11-16)

- a. Construct yeast plasmids encoding the fluorescent reporter. (Months 11-12)
- b. Evaluate fluorescent reporter with various assays in conjunction with flow cytometry quantification. (Months 12-14)
- c. Sort cells via flow cytometry to evaluate the utility of reporter gene. (Months 14-16)

Task 2: Identify PTKs from a cDNA library in yeast harboring the previously developed yeast tribrid system. (Months 16-24)

- a. Adapt and validate yeast tribrid system for use with the fluorescent reporter gene. (Months 16-19)
- b. Evaluate yeast tribrid system via flow cytometry. (Months 19-20)
- c. Co-transform yeast with a cDNA library and tribrid system to identify and isolate yeast with PTK activity via flow cytometry. (Months 20-21)
- d. Screen and sequence clones to identify active, potentially novel PTKs. (Months 22-24)

Task 3: Identify E_2 -binding proteins from a cDNA library in yeast harboring the previously developed yeast three hybrid system. (Months 24-36)

- a. Adapt and validate the yeast three hybrid system for use with the fluorescent reporter gene. (Months 24-28)
- b. Evaluate yeast three hybrid system via flow cytometry. (Months 28-30)
- c. Co-transform yeast with a cDNA library and three-hybrid system to identify and isolate yeast expressing proteins that bind E_2 . (Months 30-33)
- d. Screen and sequence clones to identify potentially novel E_2 -binding proteins.

Analysis of Protein Tyrosine Kinase Inhibitors in Recombinant Yeast Lacking the *ERG6* Gene

Daniel D. Clark and Blake R. Peterson^{*[a]}

Studies of small-molecule–protein interactions in yeast can be hindered by the limited permeability of yeast to small molecules. This diminished permeability is thought to be related to the unique sterol composition of fungal membranes, which are enriched in the steroid ergosterol. We report the construction of the novel *Saccharomyces cerevisiae* yeast strain DCY250, which is compatible with yeast two-hybrid-based systems and bears a targeted disruption of the *ERG6* gene to ablate ergosterol biosynthesis and enhance permeability to small molecules. The small-molecule inhibitors of protein tyrosine kinases (PTKs) PP1, PP2, herbimycin A, and staurosporine were investigated with yeast tribrid systems that detect the activity of the PTKs v-Abl and v-Src. These tribrid systems

function by expression of the PTK, a B42 activation domain fused to the phosphotyrosine-binding Grb2 SH2 domain, a DNA-bound LexA-GFP(AAYANAA)₄ universal PTK substrate, and a lacZ reporter gene. Yeast genetic systems that lack functional *ERG6* were found to be as much as 20-fold more sensitive to small-molecule inhibitors of PTKs than systems with *ERG6*, and these deficient systems may provide a useful platform for the discovery and analysis of small-molecule–protein interactions.

KEYWORDS:

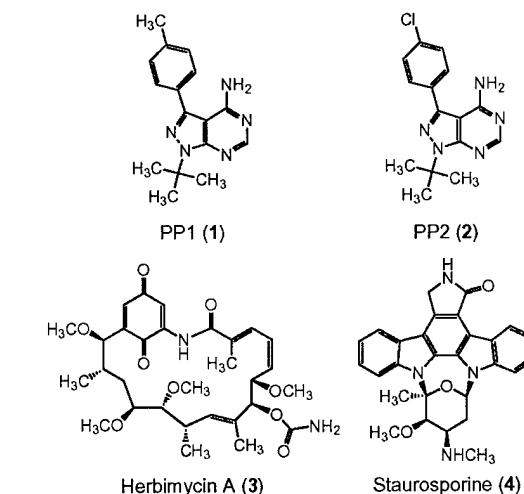
antitumor agents • high-throughput screening • molecular recognition • signal transduction • yeast

Introduction

Protein tyrosine kinase (PTK) enzymes activate complex intracellular signal transduction pathways by catalyzing the transfer of the gamma phosphoryl group of adenosine triphosphate (ATP) to tyrosine residues of target proteins. The resulting phosphotyrosine residues typically serve as docking sites for cognate phosphotyrosine-binding proteins that participate in the transmission of signals to the cell nucleus. These signals control diverse cellular functions, which include cellular proliferation, differentiation, and apoptosis.^[1, 2] Up-regulation of specific signaling pathways by members of the Abl and Src families of PTKs control the proliferation of certain cancers by activating Ras oncoproteins.^[1, 3, 4] Aberrant activation of Ras is implicated in a large number of human malignancies^[5] and PTKs therefore represent major therapeutic drug targets.^[6]

Given the importance of PTKs in human disease, novel classes of potent and selective PTK inhibitors are a widely sought after class of drug candidates (reviewed in refs. [6–8]). The majority of PTK inhibitors described to date are mimics of ATP, target the enzyme active site, and block phosphoryl transfer to target proteins. As shown in Scheme 1, this class of inhibitors includes the structurally divergent small molecules PP1 (1), PP2 (2), herbimycin A (3), and staurosporine (4).^[9–12] Although numerous inhibitors of PTK activity are known,^[6–8] the common mechanism of action of ATP mimicry has limited the identification of the highly specific compounds necessary for effective chemotherapy.^[12] Hence, novel approaches to evaluate diverse PTKs in a high-throughput screening format are sought to discover alternative types of small-molecule inhibitors.

Inhibitors of PTKs are typically investigated through evaluation of cell extracts by ELISA techniques or through analysis of



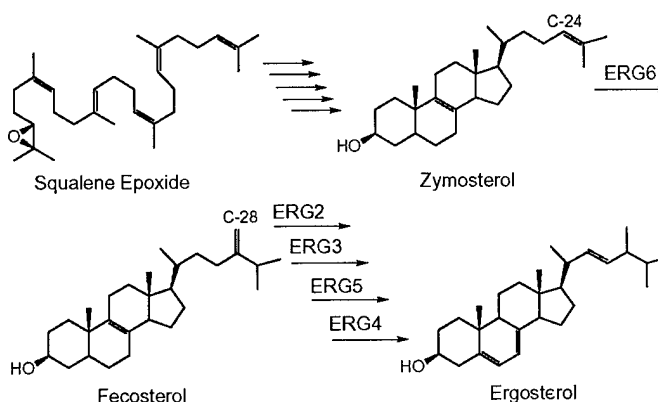
Scheme 1. Structures of protein tyrosine kinase inhibitors that engage the ATP binding site.

compounds against purified kinases in vitro.^[6] However, these methods can often be expensive and time-consuming, and often require radioactive probes. As a potentially inexpensive, rapid, and nonradioactive alternative, we are investigating the utility of

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yeast two-hybrid-based assays for detection and analysis of PTK inhibitors. Towards this end, we recently reported the construction of a yeast tribrid system that employs a potentially universal PTK substrate that is efficiently phosphorylated by the v-Abl and v-Src enzymes (Figure 1).^[13] Here, we report modifications of this yeast genetic system to enable analysis of inhibitors of this important class of enzymes.

Yeast genetic systems have emerged as powerful tools for the study of small-molecule-protein interactions (reviewed in refs. [14–17]). Recent reports have described the use of yeast one- and two-hybrid systems to investigate ligand-receptor interactions,^[18–27] and to discover inhibitors of protein-protein interactions.^[28–30] Other reports utilize yeast three-hybrid systems that employ dimeric small-molecule ligands that serve to dimerize protein ligand-binding domains and reconstitute functional transcriptional activators that activate



Scheme 2. Key elements of the yeast ergosterol biosynthetic pathway.

which has recently been attributed to increased rates of passive diffusion across cell membranes.^[50] Here, we describe analysis of PTK inhibitors in a modified yeast tribrid system that bears a targeted deletion of the *ERG6* gene carried out to enhance permeability to small molecules. Deletion of this gene was found to enable detection of specific PTK inhibitors with more than 20-fold greater sensitivity than the parent yeast strain, FY250. This approach may be useful for high-throughput identification and analysis of pharmaceutically relevant PTK inhibitors.

Results and Discussion

Targeted deletion of *ERG6* in *S. cerevisiae* strain FY250

The *ERG6* gene of yeast is critical for the biosynthesis of ergosterol.^[42] Targeted disruption of this gene to yield *erg6Δ* yeast strains can enhance permeability to a variety of small molecules.^[25, 43–50] Yet, to our knowledge, only one report has described inactivating mutations in this gene in conjunction with yeast two-hybrid assays used to detect pharmacologically relevant small molecules.^[25] We hypothesized that an *erg6Δ* yeast strain harboring the tribrid (modified two-hybrid) PTK assay shown in Figure 1 would enable improved detection of functionally diverse small-molecule inhibitors of the v-Abl and v-Src PTKs.

As shown in Figure 2, the *ERG6* gene was disrupted in yeast strain FY250 to yield the *erg6Δ* yeast strains DCY001 and DCY250. Gene deletion involved homologous recombination of a *TRP1* cassette flanked with *loxP* recombination sites into the *ERG6* locus. This insertion resulted in deletion of more than 75% of the *ERG6* gene to afford the strain DCY001. *TRP1* was chosen for selection of this initial *erg6Δ* strain because FY250 yeast are auxotrophic for tryptophan, and *trp1Δ*, *erg6Δ* strains fail to grow under normal (30 °C) aerobic culture conditions due to decreases in tryptophan uptake.^[42] However, this growth impairment is known to be obviated by aerobic culture at 37 °C.^[42] Recovery of the tryptophan selection marker by Cre-*loxP* site-specific recombination^[51] to afford strain DCY250 was found to confer this temperature-sensitive phenotype when the yeast were grown in 5–10 mL cultures under aerobic conditions. Fortu-

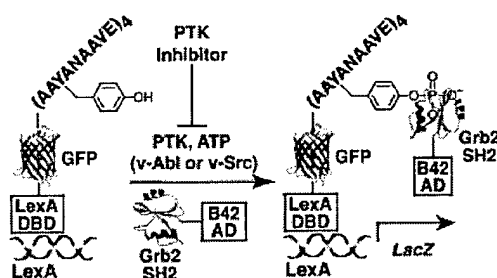


Figure 1. Schematic depiction of a yeast tribrid system incorporating a universal PTK substrate. This assay was designed to detect cell-permeable PTK inhibitors by reduction of lacZ reporter gene expression.

reporter gene expression.^[31–36] Yeast have also been recently reported as sensors for the detection of small molecules that stabilize receptor folding.^[37] However, a major limitation associated with yeast-based analysis of small molecules involves the limited permeability of yeast compared with mammalian cells.^[15] This difference in permeability has been largely attributed to differences in cellular membrane composition. Mammalian cell membranes are highly enriched in the steroid cholesterol, whereas fungal membranes substitute the structurally related steroid ergosterol (Scheme 2), which primarily differs from cholesterol by the presence of a methyl substituent on C-24. Previous studies have elucidated the components of the ergosterol biosynthetic pathway in *Saccharomyces cerevisiae*.^[38–41] As shown in Scheme 2, one particularly interesting gene in this pathway is *ERG6*, which encodes the C-24 sterol methyltransferase responsible for installation of the C-28 methyl group late in the sterol biosynthetic pathway. The *ERG6* gene product catalyzes the conversion of zymosterol to fecosterol, and deletion of *ERG6* has been shown to ablate ergosterol production without dramatically affecting cellular viability.^[42] Moreover, yeast that lack functional *ERG6* (*erg6Δ* strains) have been reported to be more permeable to small molecules,^[25, 43–50]

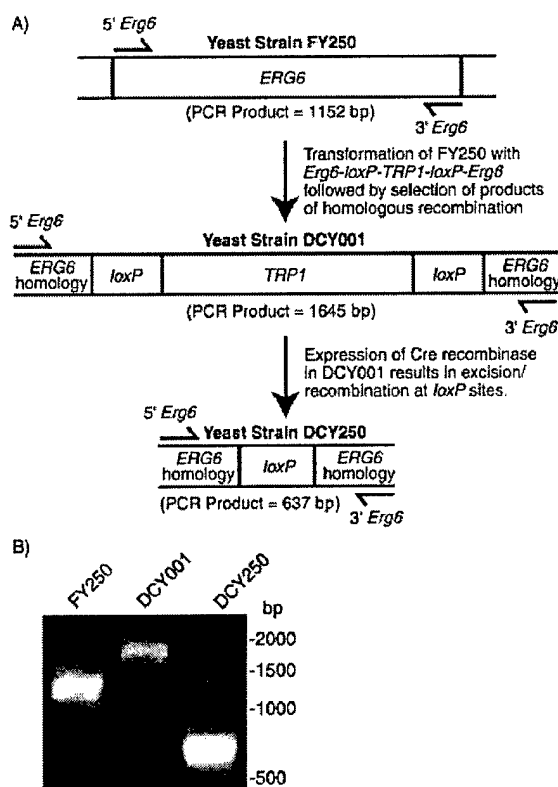


Figure 2. Disruption of the *ERG6* gene in yeast strain FY250. A) Schematic depiction of insertion of *TRP1* at the *ERG6* locus to afford strain DCY001 followed by Cre-mediated excision of *TRP1* at *loxP* sites to yield strain DCY250. B) Analytical PCR analysis of *ERG6* genes from genomic DNA of FY250, DCY001, and DCY250 yeast. (bp = base pairs).

itously however, this temperature-sensitivity was not observed with cells grown on 96-well microtiter plates under aerobic conditions at 30°C, and under these conditions growth was indistinguishable from that of the parent strain FY250. The ability of DCY250 yeast to grow on microtiter plates at 30°C enabled direct comparisons of the activities of small molecules in FY250 and DCY250 systems. These genetic modifications were validated by analytical PCR methods (Figure 2).

To compare the permeability of DCY250 and FY250 to small molecules, their sensitivity to various antimicrobial agents, such as the protein synthesis inhibitors cycloheximide and G-418, and their resistance to the antibiotic nystatin were examined. Cycloheximide and nystatin are known to exhibit differential effects on *erg6Δ* yeast strains compared with *ERG6* competent strains.^[42] As shown in Table 1, DCY250 was found to be significantly more sensitive than FY250 to the growth inhibitory effects of cycloheximide and G-418. In addition, DCY250 was substantially more resistant to nystatin, which exerts antifungal effects by binding to ergosterol in yeast membranes. These results confirmed that disruption of *ERG6* in FY250 yeast to yield DCY250 provided a yeast strain with enhanced permeability to small molecules.

Table 1. Comparison of the growth inhibition effects of antimicrobial agents on yeast strains DCY250 and FY250.^[a]

	DCY250 ^[b]	FY250 ^[b]	Fold Δ ^[c]
Cycloheximide	0.0037	0.045	12.2
G-418	1.3	22.1	17.0
Nystatin	56.9	2.6	-21.9

[a] Data shown represent the mean of duplicate experiments. Typical standard errors of the mean (SEM) were <3%. [b] Values represent concentrations (μg mL⁻¹) that inhibit growth by 50% (IC₅₀), calculated from dose-response curves. [c] Fold Δ represents growth inhibitory effects of compounds with respect to DCY250.

Modification of the yeast tribrid system

We previously reported a yeast tribrid system that detects intracellular tyrosine phosphorylation by the v-Abl and v-Src PTKs by using a universal substrate.^[13] This system was modified to facilitate the detection of small-molecule inhibitors by reducing the expression level of the two enzymes. Toward this end, the high-copy (20–50 copies per cell) episomal 2μ-origin plasmids previously employed for kinase expression were substituted with low-copy (1–2 copies per cell) centromeric plasmids (CEN4/ARS1) bearing the galactose-inducible *GAL1* promoter and *LEU2* selection marker. These low-copy kinase expression vectors were transformed into the yeast strains DCY250 and FY250 with the previously described plasmids, which express the B42-Grb2 SH2 protein, LexA-GFP-(AAYANAA)₄ protein, and a *lacZ* reporter gene.^[13] Expression of PTKs from either episomal or centromeric plasmids in tribrid assays did not result in significant differences in overall *lacZ* reporter gene expression (data not shown).

Analysis of PTK inhibitors with yeast tribrid systems

The small molecules PP1 (1), PP2 (2), herbimycin A (3), and staurosporine (4) were chosen as the known inhibitors of v-Abl and v-Src enzymes to be investigated. The former two inhibitors (1, 2) are synthetic compounds whereas the latter two (3, 4) are natural products. Literature IC₅₀ values^[52–55] for inhibition of these two enzymes are shown in Table 2. These compounds were chosen to encompass diverse functionality, such as the presence of a protonated amine at physiological pH values (staurosporine) and different molecular weights ranging from 281 daltons (PP1) to 574 daltons (herbimycin A), factors deemed likely to influence compound permeability to yeast cells.

The yeast tribrid system employed here for analysis of PTK inhibitors is illustrated schematically in Figure 1. In this system, reporter-gene expression is controlled by PTK-mediated phos-

Table 2. IC₅₀ values obtained from literature sources.^[52–55]

Inhibitor	IC ₅₀ (v-Abl)	IC ₅₀ (v-Src)
PP1 (1)	5 μM	0.3 μM
PP2 (2)	N/A	N/A
Herbimycin A (3)	5 μM	12 μM
Staurosporine (4)	80 nM	6 nM

phorylation of a LexA–GFP tetrameric universal substrate bound to DNA via the LexA DNA-binding protein. Conversion of tyrosine into phosphotyrosine in the substrate produces a high-affinity ligand of the B42-Grb2 SH2 protein, which results in recruitment of the B42 activation domain to LexA DNA binding sites of the reporter gene and activation of reporter gene expression. This gene expression should be reduced in a dose-dependent fashion by addition of a cell-permeable PTK inhibitor.

Four separate yeast tribrid assays (Figure 1) expressing the v-Abl or v-Src PTKs in FY250 or DCY250 (*erg6Δ*) yeast were investigated with the PTK inhibitors shown in Scheme 1. These inhibitors were also analyzed with control yeast strains that constitutively activate reporter gene expression by expression of a LexA–B42 fusion protein. These control experiments enabled nonspecific effects on reporter gene expression to be distinguished from specific effects on tyrosine kinase activity. As shown in Figure 3, dose-dependent effects of inhibitors on reporter gene expression were quantified, and IC_{50} values were determined (Table 3).

The results shown in Figure 3 and Table 3 demonstrate that deletion of the *ERG6* gene renders the DCY250 yeast strain substantially more sensitive to PTK inhibitors than strain FY250. Whereas only the low-molecular-weight PP1 (1) and PP2(2)

Table 3. IC_{50} values measured in yeast systems.^[a]

Inhibitor	DCY250 Yeast			FY250 Yeast		
	v-Abl	v-Src	LexA–B42	v-Abl	v-Src	LexA–B42
PP1 (1)	12	7.6	>100	20	>100	>100
PP2 (2)	4.2	4.5	>100	25	>100	>100
Herbimycin A (3)	5.2	0.58	>10	>10	>10	>10
Staurosporine (4)	4.4	3.1	>10	>10	>10	>10

[a] Values represent concentrations (μ M) required to inhibit reporter gene expression in yeast PTK tribrid assays by 50% (IC_{50}), calculated from the data shown in Figure 3.

compounds had significant effects against FY250, all of the inhibitors (1–4) conferred dose-dependent reductions in reporter gene expression in the *ERG6*-deficient DY250 strain. Importantly, all four inhibitors exhibited only minor effects on the control LexA–B42 assay at the highest concentrations examined (Table 3). Remarkably, although herbimycin A exhibits the lowest potency in vitro (Table 2) and is of the highest molecular weight, this compound proved to be the most potent compound against the DCY250 PTK assays. Herbimycin A was approximately 20 times more potent in the DCY250 strain than in FY250. This observation may relate to irreversible inhibition of PTKs by this compound.^[11] In contrast, the other compounds (1–3) are reversible PTK inhibitors.

The effects of compounds 1–4 on yeast growth were quantified in order to examine whether inhibition of cellular growth might contribute to effects on reporter gene expression. In these experiments (Table 4) cells were grown in the presence of test compounds for 16 hours and cell density was determined from absorbance values. Over this time interval, the growth of DCY250 was affected by all of the inhibitors, but most profoundly by staurosporine (3), which was highly toxic to both DCY250 and FY250. However, these effects on cellular growth are not likely to significantly influence the inhibitor data shown in Figure 3 and Table 3 because the inhibitors were analyzed after treatment of yeast for only 4 hours. This conclusion is supported by comparison with the corresponding control experiments with the LexA–B42 fusion protein.

To confirm that inhibitors 1–4 influence the activity of PTKs in whole yeast cells, the DCY250 strain that expresses v-Src was analyzed by immunoblotting with antiphosphotyrosine (Figure 4). These experiments re-

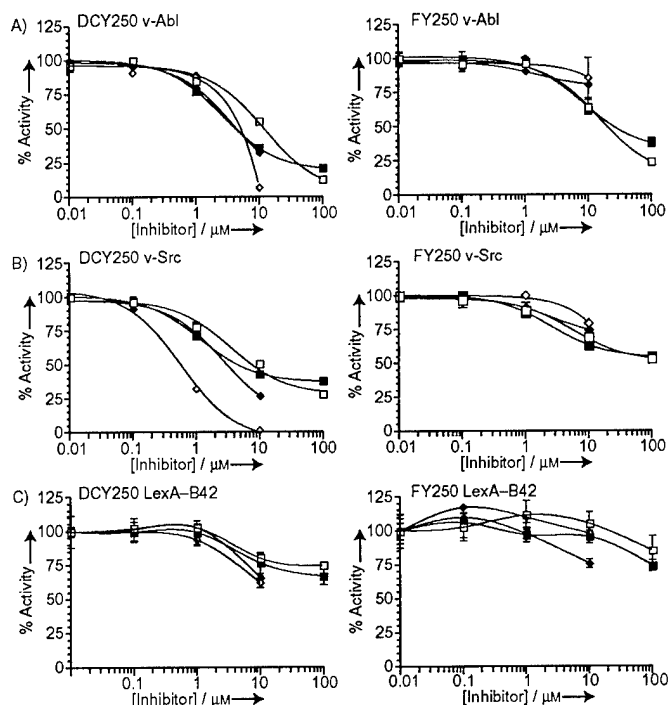


Figure 3. Dose–response curves for yeast genetic systems treated with inhibitors □ PP1(1), ■ PP2(2), ○ Herbimycin A(3), and ● Staurosporine (4). A) Expression of v-Abl in DCY250 (left) and FY250 (right) yeast tribrid systems. B) Expression of v-Src in yeast tribrid systems. C) Control yeast one-hybrid systems that constitutively activate reporter gene expression of a LexA–B42 fusion. Percentage activity represents normalized data with respect to the lowest concentration of inhibitor shown. Data presented are the average of at least duplicate experiments. Error bars represent SEM values. Typical errors were <5%.

Table 4. Inhibition of yeast growth by PTK inhibitors.^[a]

	% Inhibition of growth	
	DCY250	FY250
PP1 (1, 100 μ M)	78	0
PP2 (2, 100 μ M)	43	0
Herbimycin A (3, 10 μ M)	30	0
Staurosporine (4, 10 μ M)	100	95

[a] Data shown represent the mean of duplicate experiments with typical SEM values of <1%.

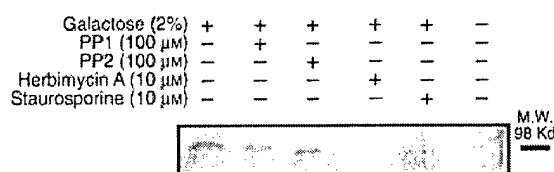


Figure 4. Immunoblot analysis of the DCY250 v-Src tribrid assay by detection of phosphorylated proteins with antiphosphotyrosine. Each lane was loaded with equivalent amounts of cell extract after treatment with inhibitor for 4 hours.

vealed that all of the inhibitors reduce v-Src activity and herbimycin A (10 μ M) confers the greatest effect on phosphorylation. These results are consistent with the transcriptional tribrid dose-response data from Figure 3 and Table 3.

The results presented here demonstrate that yeast strains without the *ERG6* gene can be employed in two-hybrid-based assays to identify pharmacologically relevant small molecules that are normally impermeable to yeast. Given the importance of protein tyrosine kinases in human disease, the modified yeast tribrid assays reported here may be useful for the discovery of drug leads in high-throughput screening assays.

Experimental Section

General: Standard techniques for plasmid construction,^[56] yeast transformation,^[57] and amplification of yeast genomic DNA^[58] were employed. The compounds PP1, PP2, and G-418 were obtained from Calbiochem. Herbimycin A, staurosporine, cycloheximide, nystatin, and dimethyl sulfoxide (DMSO) were purchased from Sigma-Aldrich. 5-Fluoroorotic acid (5-FOA) was purchased from Toronto Research Inc. DNA oligonucleotides were from Integrated DNA Technologies. Restriction endonucleases and deoxynucleotide triphosphates were from New England Biolabs. GeneChoice *Taq* polymerase was purchased from PGC Scientific, and *Pfu* polymerase was purchased from Stratagene. DNA isolation and purification kits were from Qiagen. Microbiological media were from Difco and qBiogene. Prepacked solid yeast selection media was purchased from KD Medical. All new DNA constructs were confirmed by automated dideoxynucleotide sequencing at the Pennsylvania State University Nucleic Acid Facility. Data analysis was performed with the GraphPad Prism 3.0 program (GraphPad Software, Inc. San Diego, CA).

Bacterial and yeast strains: *Escherichia coli* DH5- α (Clontech) was employed for plasmid construction. *Saccharomyces cerevisiae* FY250 (*MAT α* , *ura3*-52, *his3 Δ 200*, *leu2 Δ 1*, *trp1 Δ 63*) was a generous gift of Prof. M. Ptashne (Memorial Sloan-Kettering). Yeast strains DCY001 (*MAT α* , *ura3*-52, *his3 Δ 200*, *leu2 Δ 1*, *trp1 Δ 63*, *erg6:loxP-TRP1-loxP*) and DCY250 (*MAT α* , *ura3*-52, *his3 Δ 200*, *leu2 Δ 1*, *trp1 Δ 63*, *erg6:loxP*) were constructed as described within this study.

Plasmid construction: The yeast tribrid plasmids pJG4-5 Grb2 SH2, pAMLexA2 GFP-(AAYANAA)₄, pAMLexA2 GFP-(AAFANAA)₄, and the reporter vector pSH18-34 were described previously.^[13] To reduce the expression levels of the v-Abl (amino acids 237-630) and v-Src (amino acids 137-526) PTKs, these genes were expressed from vector pYCDC. pYCDC is a *GAL1*-inducible, *LEU2*-selectable, centromeric plasmid constructed from pYCplac111^[59] (a gift from R. D. Gietz) by digestion with *EcoRI*/*HindIII* and ligation to a *MfeI*-*GAL1* promoter-HA tag-*EcoRI*/*XhoI*-ADH1 terminator-*HindIII* (HA = hemagglutinin epitope tag) fragment derived from pRF4-6, a derivative of

pJG4-5^[60] that lacks the B42 activation domain and SV40 nuclear localization sequence^[61]. The control plasmid for expression of the constitutively active LexA-B42 AD fusion protein was prepared by ligation of a *MfeI*-SV40 NLS-B42 AD-HA tag-*XhoI* fragment derived from pJG4-5^[60] into pAM423LexA.^[13]

PCR from the template plasmid pDC2 *ERG6-loxP2-TRP1-ERG6* generated the disruption cassette used to construct yeast strain DCY001. This plasmid included *loxP* sites amplified by PCR from the plasmid pU6H3HA^[62] (a gift from A. De Antoni) and cloned into pDC2^[13] to afford pDC2 *loxP2*. The forward *loxP* site included the hexameric 6 \times His and trimeric HA tag sequences of pU6H3HA^[62] flanked by in-frame 5' *KpnI* and 3' *MfeI* restriction sites. The reverse *loxP* site was amplified to include flanking in-frame 5' *XhoI* and 3' *PstI* restriction sites. The *ERG6* gene sequences of the disruption cassette were generated by PCR amplification of yeast genomic DNA. Homology to N-terminal *ERG6* sequences included 270 bp upstream and 129 bp downstream of the *ERG6* start codon, flanked by in-frame 5' *BamHI* and 3' *KpnI* restriction sites. Homology to C-terminal *ERG6* sequences included 129 bp upstream and 270 bp downstream of the *ERG6* stop codon, flanked by in-frame 5' *PstI* and 3' *HindIII* restriction sites. These *ERG6* gene fragments were cloned into pDC2 *loxP2* to create pDC2 *ERG6-loxP2-ERG6*. The *TRP1* selection marker was amplified from pJG4-5^[60] flanked by in-frame 5' *EcoRI* and 3' *XhoI* restriction sites and cloned into *EcoRI*/*XhoI*-digested pDC2 *ERG6-loxP2* to afford the final disruption template.

Targeted disruption of *ERG6*: Yeast strain FY250 was transformed with a DNA cassette amplified by PCR from plasmid pDC2-*ERG6-loxP2-TRP1-ERG6* to include 149 bp of *ERG6* homology flanking each of the *loxP* sites. Homologous recombination yielded colonies that grew on solid synthetic-defined (SD) media (2% glucose) that lacked tryptophan (*trp*⁻). Isolation and PCR analysis of individual yeast colonies provided the DCY001 strain.

DCY001 was transformed with the *Cre* expression plasmid pSH47^[51] and transformants were selected on solid SD media (2% glucose) lacking uracil (*ura*⁻) and tryptophan (*trp*⁻). Selected transformants were inoculated into liquid yeast peptone media (2% galactose, YPGal) to induce *Cre* recombinase expression and incubated with shaking at 30°C for 17 hours. Approximately 500 yeast cells were plated on solid SD media (2% glucose, *ura*⁻) and incubated at 30°C for 6 days. The most well-defined colonies were patched to solid SD media (2% glucose, *trp*⁻, *ura*⁻) to verify auxotrophic markers, and to solid SD media (2% glucose, *ura*⁻) for further analysis, and were incubated at 37°C for 1 day. Analytical PCR identified colonies with the appropriate genomic mutations. These colonies were patched to 5-FOA (1 mg mL⁻¹) plates and incubated at 37°C for 2 days to remove the pSH47^[51] plasmid. The resulting colonies were patched to solid yeast peptone media (2% dextrose, YPD) to obtain single colonies for final PCR analysis. A colony was selected based on PCR analysis and good growth characteristics and was patched to solid SD media (2% glucose, *ura*⁻) and solid SD media (2% glucose, *trp*⁻) and incubated at 37°C to confirm auxotrophic markers. The strain derived from this colony was named DCY250. It should be noted that some of the media described above were supplemented with ergosterol (0.02 mg mL⁻¹ final concentration added from a 1:1 ethanol/tergitol NP-40 200X stock solution) in an attempt to improve growth characteristics at 30°C. However, aerobically cultured yeast cannot incorporate exogenously supplied ergosterol^[38, 39] and ergosterol supplementation is not likely to have influenced yeast growth.

Yeast tribrid β -galactosidase reporter gene assay: Yeast tribrid assays for *S. cerevisiae* FY250 and DCY250 yeast were performed essentially as described previously.^[13] Briefly, yeast harboring the appropriate plasmids were grown for 16 hours in SD liquid media

(2% raffinose, ura⁻, trp⁻, his⁻, leu⁻). Aliquots of saturated yeast cultures (80 µL) were added to a sterile 96-well microtiter plate followed by SD liquid media (100 µL, 4% galactose, ura⁻, trp⁻, his⁻, leu⁻) with a 10X stock solution of the PTK inhibitor (20 µL, 10% DMSO in H₂O). The plate was incubated with shaking at 30°C for 4 hours and assayed for β -galactosidase reporter gene activity as previously described.^[13] Values reported here represent the mean of at least duplicate experiments and were normalized to the activity calculated for wells containing the lowest concentration of the inhibitor shown. IC₅₀ values were calculated by nonlinear regression with a one-site competition model (GraphPad Prism 3.0 software). Side-by-side comparisons with a nonphosphorylated phenylalanine analogue of the universal substrate (LexA-GFP-(AAFANAA)₄) typically provided less than 5% of the activity of the tyrosine-containing universal substrate. Error bars in the figures represent standard errors of the mean.

Immunoblotting: Yeast colonies picked for the DCY250 v-Src tribrid assays were grown 16 hours in SD media (2% raffinose, ura⁻, trp⁻, his⁻, leu⁻) and aliquotted (0.8 mL) onto a 24-well plate containing SD media (0.1 mL, 20% galactose, ura⁻, trp⁻, his⁻, leu⁻) and PTK inhibitors (0.1 mL, 10X stocks in 10% DMSO in H₂O) then incubated with shaking at 30°C for 4 hours. Preparation of cell lysates and immunoblotting was performed as previously described,^[13] but the immunoblots were developed with a CN/DAB substrate (Pierce).

Evaluation of growth inhibition: The growth inhibitory effects of compounds on FY250 or DCY250 yeast strains were determined by calculating the change in cell density after incubation with compounds for 16 hours. Briefly, aliquots of freshly inoculated YPD media (157.5 µL) and compounds (17.5 µL, 10X stocks in 10% DMSO in H₂O) were arrayed on 96-well plates and the initial cell density was determined by absorbance measurements at 590 nm. The plates were incubated with shaking at 30°C for 16 hours and the final cell density was determined. Cell growth was calculated as the difference in cell densities. Values reported represent the mean of duplicate experiments and were normalized to cell growth in control wells (1% DMSO). IC₅₀ values were calculated by nonlinear regression with a sigmoidal dose-response model (GraphPad Prism 3.0 software). Errors quoted correspond to standard errors of the mean.

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